

Raw Sequence Listing before editing (for reference only)



PCT

RAW SEQUENCE LISTING

DATE: 05/19/2006

PATENT APPLICATION: US/10/521,518

TIME: 08:56:38

Input Set : A:\294-208 PCT-US sequence listing.txt

Output Set: N:\CRF4\05192006\J521518.raw

3 <110> APPLICANT: Expressive Research B.V.
 5 <120> TITLE OF INVENTION: Modulating developmental pathways in plants
 7 <130> FILE REFERENCE: P59845PC00
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/521,518
 C--> 10 <141> CURRENT FILING DATE: 2005-01-18
 12 <150> PRIOR APPLICATION NUMBER: EP 02077908.8
 13 <151> PRIOR FILING DATE: 2002-07-17
 15 <160> NUMBER OF SEQ ID NOS: 110
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 227
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Arabidopsis thaliana
 24 <400> SEQUENCE: 1
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 27 1 5 10 15
 30 Pro Pro Pro Ala Pro Lys Gly Tyr Tyr Arg Arg Gly His Gly Arg Gly
 31 20 25 30
 34 Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu
 35 35 40 45
 38 Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
 39 50 55 60
 42 Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
 43 65 70 75 80
 46 Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
 47 85 90 95
 50 Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
 51 100 105 110
 54 Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr
 55 115 120 125
 58 Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
 59 130 135 140
 62 Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
 63 145 150 155 160
 66 Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
 67 165 170 175
 70 Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
 71 180 185 190
 74 Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr
 75 195 200 205
 78 Ser Asn Gly Thr Thr Thr Thr Ser Thr Val Phe Pro Ile Lys Cys Asp
 79 210 215 220
 82 Phe Asp Phe

pp 7-9
 Does Not Comply
 Corrected Diskette Needed

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83 225
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 416
88 <212> TYPE: PRT
89 <213> ORGANISM: Arabidopsis thaliana
91 <400> SEQUENCE: 2
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97 Thr His Phe Asp Leu Glu Ser Asn Asn Asn Leu Gln Tyr Ser Leu Ser
98          20          25          30
101 Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr
102          35          40          45
105 Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala
106          50          55          60
109 Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu
110 65          70          75          80
113 Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu
114          85          90          95
117 Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp
118          100          105          110
121 Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr
122          115          120          125
125 Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala
126          130          135          140
129 Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile
130 145          150          155          160
133 Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu
134          165          170          175
137 Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala
138          180          185          190
141 Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala
142          195          200          205
145 Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro
146          210          215          220
149 Lys Gly Ser Phe Ser Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser
150 225          230          235          240
153 Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu
154          245          250          255
157 Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu
158          260          265          270
161 Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met
162          275          280          285
165 Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp
166          290          295          300
169 Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys
170 305          310          315          320
173 Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu
174          325          330          335
177 Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Phe Leu Ser Gly Asp Leu

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178          340          345          350
181 Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr
182          355          360          365
185 Arg Arg Lys Ala Trp Cys Glu Glu Glu Asp Glu Glu Gln Arg Lys Lys
186          370          375          380
189 Gln Gln Lys Lys Lys Thr Met Ser Glu Lys Arg Arg Arg Glu Glu Lys
190 385          390          395          400
193 Lys Val Asn Lys Pro Asn Gly Phe Val Phe Cys Val Leu Gly His Lys
194          405          410          415
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1634
199 <212> TYPE: DNA
200 <213> ORGANISM: Arabidopsis thaliana
203 <220> FEATURE:
204 <221> NAME/KEY: CDS
205 <222> LOCATION: (501)..(563)
206 <223> OTHER INFORMATION: signal sequence (exon 1)
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (655)..(708)
211 <223> OTHER INFORMATION: propeptide (exon 2)
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (797)..(856)
216 <223> OTHER INFORMATION: propeptide (exon 3)
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (955)..(1131)
221 <223> OTHER INFORMATION: conserved cysteine motif (exon 4)
223 <400> SEQUENCE: 3
224 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat      60
226 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac      120
228 ataaactacc aaagtatcaa gctaattgtaa aaattactct catttccacg taacaaattg      180
230 agtttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcac      240
232 ctccgaaaaa aggggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca      300
234 aatgcaatct ataactctgtg atttatccaa taaaaacctg tgatttatgt ttgggtccag      360
236 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa      420
238 gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc      480
240 aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg      533
241          Met Lys Lys Met Asn Val Val Ala Phe Val Thr
242          1          5          10
244 ctg atc atc tct ttt ctt ctg ctt tct cag gtaaactgtt aaaaccattt      583
245 Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln
246          15          20
248 tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg      643
250 gtctttcata g gta ctt gca gag ttg tca tca tcc agc aac aat gaa act      693
251          Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn Glu Thr
252          25          30
254 tcc tct gtt tct cag gtaagagtga tacaaaaaca tactaaacaa actttcaaga      748

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255 Ser Ser Val Ser Gln
256 35
258 gagtaatata taaggaaatg ttggcttctt ttttttgttg ctaatcag acg aat gac      805
259                                     Thr Asn Asp
260                                     40
262 gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga      853
263 Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg
264      45      50      55
266 atc agttagtcta ctctttcaac actctaattc ctttgttcta agtatttttt      906
267 Ile
270 ttgcccccca caaccttttt tttattaaat gagccaattt ttatagat tgt ggg cat      963
271                                     Cys Gly His
272                                     60
274 gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac      1011
275 Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His
276      65      70      75
278 aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga      1059
279 Arg Ala Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly
280      80      85      90
282 acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca      1107
283 Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr
284 95      100      105      110
286 cat ggc aat aaa ctg aaa tgt cct taaaagactt ctcatctctc aactatagtc      1161
287 His Gly Asn Lys Leu Lys Cys Pro
288      115
290 tcattcttctg attatgtttc ttcttttggt atgttgcatg tgtgatgtgt gagcttatta      1221
292 ttatgttgat tgttgacata attcaactat ataatttgta tcgattccga ataataagat      1281
294 gagtgattttt attggctatt aagttttttt tttttttttt tgggcacaat ggctattaag      1341
296 ttttaaacaat ctgattttat tggttacaaa aaacaacaaa gtttcatttt catattaaca      1401
298 caaaatctcc atacatatta ccaaaccaaa aaaatacaca aggggggagag agaccaacgg      1461
300 ttcttggttc agagtttgca tcttgtttga gccgtcacccg tttcttagac ttaacagcca      1521
302 caacaccttt ataaagcttc acgcgatcct tcaacgcatt tcgccgaggc cgagccacct      1581
304 tattgttttg atcaaacaac aaaacttctt caaacgcatt caatgccaaa ggc      1634
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 118
309 <212> TYPE: PRT
310 <213> ORGANISM: Arabidopsis thaliana
312 <400> SEQUENCE: 4
314 Met Lys Lys Met Asn Val Val Ala Phe Val Thr Leu Ile Ile Ser Phe
315 1      5      10      15
318 Leu Leu Leu Ser Gln Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn
319      20      25      30
322 Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala
323      35      40      45
326 Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys
327      50      55      60
330 Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala
331 65      70      75      80
334 Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser

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335          85          90          95
338 Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr His Gly
339          100          105          110
342 Asn Lys Leu Lys Cys Pro
343          115
346 <210> SEQ ID NO: 5
347 <211> LENGTH: 1453
348 <212> TYPE: DNA
349 <213> ORGANISM: Arabidopsis thaliana
352 <220> FEATURE:
353 <221> NAME/KEY: CDS
354 <222> LOCATION: (501)..(533)
355 <223> OTHER INFORMATION: signal peptide (exon 1)
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (664)..(691)
360 <223> OTHER INFORMATION: propeptide (exon 2)
362 <220> FEATURE:
363 <221> NAME/KEY: CDS
364 <222> LOCATION: (772)..(950)
365 <223> OTHER INFORMATION: conserved cysteine motif (exon 3)
367 <400> SEQUENCE: 5
368 gaaaaaaaga agaaaagata atgggtccgta ttaatatagt tgaaaacttg aaactacttt      60
370 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag      120
372 tttgtgttta tgtttgattt tacgttttta tatgtaaata agatatttta cgaattatgg      180
374 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat      240
376 aaagtaatat aatatatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac      300
378 acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa      360
380 atctctcaaa gtaagaacta agagctttac tacagtecta ctctctacac atcttctctc      420
382 tctctcaaga gctagtcatg gccaaactca taacttcttt tctcttactc acaattttat      480
384 tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt      533
385          Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser
386          1          5          10
388 gtaagttttt attttttggg aaaatagaaa gtgtaagttt tataattcat tcaattgttt      593
390 ttgcctttcc ctttctattt attgctataa atctaatacc cgcgttaaaa tttgttttga      653
392 aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa      701
393          Tyr Gly Pro Gly Ser Leu Lys Ser Tyr
394          15          20
396 acttcttctt cttttatgaa tcttgtttct tattatatat caaataaaaa ctcgattatc      761
398 atgattgcag aa tgt gga gga caa tgc aca agg aga tgt agc aac aca      809
399          Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn Thr
400          25          30
402 aag tat cat aag cca tgc atg ttc ttc tgc caa aag tgt tgt gct aaa      857
403 Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala Lys
404          35          40          45
406 tgc ctt tgt gtc cct cca ggc acg tac ggc aac aaa caa gtg tgt cct      905
407 Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro
408 50          55          60          65
410 tgt tac aac aac tgg aag act caa caa ggt gga cca aaa tgt cca      950

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/19/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 2,4,7,8,9,10,11,12,13,14,16,17,18,20,21,24,25,27,31,34,36

Seq#:31; Xaa Pos. 37,38,39,41,44,45,46,47,48,49,50,52,53

from seq. 19

7

gtc ggt gaa ggc gta gtg aaa att g gatatgtaacg ctaacatata 739
Val Gly Glu Gly Val Val Lys Ile
35

tgttaaagtgt tataatctctg tttatatatg atttttaaac ggtaaaaaac tagtcatatg 799

tgtataaata tatcatgtga ag at tgc ggt ggg aga tgc aaa ggt aga tgc 850
Asp Cys Gly Gly Arg Cys Lys Gly Arg Cys
45

insert → 40

agc aaa tcg tcg agg cca aat ctg tgt ttg aga gca tgc aac agc tgt 898
Ser Lys Ser Ser Arg Pro Asn Leu Cys Leu Arg Ala Cys Asn Ser Cys
50 55 60 65

tgt tac cgc tgc aac tgt gtg cca cca ggc acc gcc ggg aac cac cac 946
Cys Tyr Arg Cys Asn Cys Val Pro Pro Gly Thr Ala Gly Asn His His
70 75 80

ctt tgt cct tgc tac gcc tcc att acc act cgt ggt ggc cgt ctc aag 994
Leu Cys Pro Cys Tyr Ala Ser Ile Thr Thr Arg Gly Gly Arg Leu Lys
85 90 95

tgc cct taaacatata cacatacaga tgtgtgtata tgtcttccgc gagcacacac 1050
Cys Pro

from. seq. 21

8

ggt gaa ggc gta gtg aaa atc g gtagtgaacc ctaacttata tataacacgt 745
Gly Glu Gly Val Val Lys Ile
35

tggtatataa cttaatatct ctgatgggtg cactctcttc ccaacttata tataatcttg 805

ttatggagaa tgtctcaagc ttttaatgag atgttatatc toggagaagg aaactatgaa 865

ctaaaagcctt tggattcctt tgcaacaaat ataaactttt gatgggttta aacggattaa 925

attagttaca tgtgtttgat gaatgtatgt atgattgtag at tgt ggt ggg aga 979
Asp Cys Gly Gly Arg

insert 40

tgc aaa gat aga tgc agc aaa tct tcg aga acg aag cta tgc ttg aga 1027
Cys Lys Asp Arg Cys Ser Lys Ser Ser Arg Thr Lys Leu Cys Leu Arg
45 50 55 60

gcg tgc aac agc tgt tgt tcc cgc tgc aac tgt gtg cca cct ggt act 1075
Ala Cys Asn Ser Cys Cys Ser Arg Cys Asn Cys Val Pro Pro Gly Thr
65 70 75

tct gga aac acc cac ctt tgt cct tgc tac gcc tcc att acc act cac 1123
Ser Gly Asn Thr His Leu Cys Pro Cys Tyr Ala Ser Ile Thr Thr His
80 85 90

ggt ggc cgc ctc aag tgc cct taaaatttct tctgtgtctg tttctgtttc 1174
Gly Gly Arg Leu Lys Cys Pro
95

from seq. 25

9

gcg ccg cct gtc aaa cct cca aca cca cct ccc gta aga act cgg ata g 1391
Ala Pro Pro Val Lys Pro Pro Thr Pro Pro Pro Val Arg Thr Arg Ile
200 205 210

gtaataataa ttttctttca aaagtgtgat gattatcggc cggttgattag atcggatgta 1451

taattggact aaattttgga cggttttag at tgc gtg cct tta tgt ggg acg 1502
Asp Cys Val Pro Leu Cys Gly Thr
mut → 215 220

agg tgt ggg caa cac tcg agg aag aac gta tgt atg aga gcg tgc gtc 1550
Arg Cys Gly Gln His Ser Arg Lys Asn Val Cys Met Arg Ala Cys Val
225 230 235

acg tgc tgc tac cgc tgc aag tgt gtt ccc cca ggc acc tac ggt aat 1598
Thr Cys Cys Tyr Arg Cys Lys Cys Val Pro Pro Gly Thr Tyr Gly Asn
240 245 250

aag gag aag tgt gga tct tgt tac gcc aac atg aag aca cgt ggt gga 1646
Lys Glu Lys Cys Gly Ser Cys Tyr Ala Asn Met Lys Thr Arg Gly Gly
255 260 265 270

aaa tcc aaa tgt cct tgaaccttta tatgacgatg gttgttaaac gaaataattt 1701
Lys Ser Lys Cys Pro
275

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:517 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1047 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 15
L:1311 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:1312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1448 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:1786 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:2187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:2191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:16
L:2195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:32
L:2199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:48